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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Daggett, Lorrie P.
Ellis, Steven B.
Liaw, Chen W.
Lu, Chin-Chun
- (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING SAME AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 21

- (iv) CORRESPONDENCE ADDRESS:
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- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 20-APR-1994
(C) CLASSIFICATION:

- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/052,449
(B) FILING DATE: 20-APR-1993

- (viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 262..3078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGCG GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC Met Ser Thr Met Arg Leu Leu Thr Leu Ala	291
1 5 10	
CTG CTG TTC TCC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	339
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	387
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	435
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	483
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	531
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	579
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	627
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	675
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	723
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	771
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	819
175 180 185	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	867
190 195 200	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	915
205 210 215	

ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220 225 230	963
GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly 235 240 245 250	1011
GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile 255 260 265	1059
CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser 270 275 280	1107
GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys 285 290 295	1155
GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile 300 305 310	1203
TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr 315 320 325 330	1251
GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg 335 340 345	1299
AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val 350 355 360	1347
CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys 365 370 375	1395
ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG Ile Ile Trp Pro Gly Gly Thr Glu Lys Pro Arg Gly Tyr Gln Met 380 385 390	1443
TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr 395 400 405 410	1491
GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Phe Thr Val 415 420 425	1539
AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr 430 435 440	1587
TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe 445 450 455	1635
TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr 460 465 470	1683
GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val 475 480 485 490	1731

AAC AAC AGC AAC AAG GAG TGG AAT CGG ATG ATG GGC GAG CTG CTC Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu 495 500 505	1779
AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu 510 515 520	1827
CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu 525 530 535	1875
ACT ATT CTG GTC AAG AAG GAG ATT CCC CCG AGC ACG CTG GAC TCG TTC Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe 540 545 550	1923
ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val 555 560 565 570	1971
CAC GTG GTG GCC CTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe 575 580 585	2019
GCG CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr 590 595 600	2067
CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly 605 610 615	2115
ATC GGG GAA GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met 620 625 630	2163
GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn 635 640 645 650	2211
CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly 655 660 665	2259
ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala 670 675 680	2307
ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu 685 690 695	2355
CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala 700 705 710	2403
GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile 715 720 725 730	2451
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu 735 740 745	2499
GTG ACC ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met 750 755 760	2547

CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 765 770 775	2595
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg 780 785 790	2643
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 795 800 805 810	2691
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 815 820 825	2739
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp 830 835 840	2787
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp 845 850 855	2835
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870	2883
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 875 880 885 890	2931
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC Phe Lys Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Arg Arg 895 900 905	2979
GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile 910 915 920	3027
GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser 925 930 935	3075
TGAGACTCCC CGCCCCGCCCT CCTCTGCCCT CTCCCCCGCA GACAGACAGA CAGACGGACG	3135
GGACAGCGGC CGGGCCCACG CAGAGCCCCG GAGCACCAACG GGGTCGGGGG AGGACCAACCC	3195
CCAGCCTCCC CCAGGCTGCC CCTGCCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC	3255
GTCCCCGGCCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTCT	3315
ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCCC TCAACCTCTC AGATCCCTCG	3375
GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCCCACCTG CCCAGTTAGC CCGGCCAAGG	3435
ACACTGATGG GTCTGCTGC TCGGGAAAGGC CTGAGGGAAAG CCCACCCGCC CCAGAGACTG	3495
CCCACCCCTGG GCCTCCCCTC CGTCCGCCCG CCCACCCCGC TCCCTGGCCG GCAGCCCCCTG	3555
CTGGACCAAG GTCGGGACCG GACCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGGCAG	3615
GGCCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG	3675
GCTAACTGCC CCCAGGCCGA GGGGCTTGGA GCAGAGACGG CAGCCCCATC CTTCCCGCAG	3735
CACCAGCCTG AGCCACAGTG GGGCCCATGG CCCCCAGCTGG CTGGTGCCTC CCTCCTCGGG	3795

CGCCTGCCGT CCTCTGCAGC CTGAGCTCCA CCCTCCCCCTC TTCTTGCGGC ACCGCCACC	3855
AAACACCCCG TCTGCCCTT GACGCCACAC GCCGGGGCTG GCGCTGCCCT CCCCCCACGGC	3915
CGTCCCTGAC TTCCCAGCTG GCAGCGCCTC CGGCCGCCCTC GGGCCGCCTC CTCCAGAATC	3975
GAGAGGGCTG AGCCCCTCCT CTCCTCGTCC GGCCCTGCAGC ACAGAAGGGG GCCTCCCCGG	4035
GGGTCCCCGG ACCCTGGCTC GGGACTGTCT TCAACCCCTGC CCTGCACCTT GGGCACGGGA	4095
GAGCGCCACC CGCCGCCCG CGCCCTCGCT CCGGGTGCCT GACCGGCCCG CCACCTTGTA	4155
CAGAACCAAGC ACTCCCAGGG CCCGAGCGCC TGCCCTCCCC GTGCGCAGCC GCGCTCTGCC	4215
CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCCAACCCCCC ACCTCCCGGT GTATGCAGTG	4275
GTGATGCCTA AAGGAATGTC ACG	4298

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 938 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala	
165 170 175	
Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu	
180 185 190	

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu
 195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser
 210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met
 225 230 235 240

Gly Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Gly Ile Ser
 245 250 255

Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile
 260 265 270

Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val
 275 280 285

Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro
 290 295 300

Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu
 305 310 315 320

Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly
 325 330 335

Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser
 340 345 350

Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn
 355 360 365

Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly
 370 375 380

Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile
 385 390 395 400

Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser
 405 410 415

Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys
 420 425 430

Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg
 435 440 445

His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile
 450 455 460

Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala
 465 470 475 480

Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys
 485 490 495

Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met
 500 505 510

Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu
 515 520 525

Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys
 530 535 540

Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser
 545 550 555 560
 Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met
 565 570 575
 Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn
 580 585 590
 Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp
 595 600 605
 Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro
 610 615 620
 Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala
 625 630 635 640
 Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val
 645 650 655
 Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu
 660 665 670
 Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser
 675 680 685
 Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg
 690 695 700
 His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala
 705 710 715 720
 Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu
 725 730 735
 Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu
 740 745 750
 Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp
 755 760 765
 Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe
 770 775 780
 Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser
 785 790 795 800
 Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val
 805 810 815
 Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe
 820 825 830
 Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met
 835 840 845
 Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp
 850 855 860
 Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe
 865 870 875 880
 Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser
 885 890 895

Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg Gly Ala Leu Gln Asn Gln
 900 905 910

Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln
 915 920 925

Leu Gln Leu Cys Ser Arg His Arg Glu Ser
 930 935

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:-

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG TCC TAT GAC AAC	48
Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn	
1 5 10 15	

AAG CGC GGA CCC AAG	63
Lys Arg Gly Pro Lys	
20	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn	
1 5 10 15	

Lys Arg Gly Pro Lys	
20	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 189..3899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCTTAATAA GATTTGCCAC GTACACTCGA GCCATCGCGA GTGTCCCTGA	GGCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT	GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCCG	AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC		230
Met Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu		
1 5 10		
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG		278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met		
15 20 25 30		
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC		326
Thr Val Ala Val Phe Ser Ser Gly Pro Pro Gln Ala Gln Phe		
35 40 45		
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC		374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile		
50 55 60		
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC		422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu		
65 70 75		
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC		470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val		
80 85 90		
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC		518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe		
95 100 105 110		
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT		566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser		
115 120 125		
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG		614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu		
130 135 140		
GGC GTG TCC CTG GAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA		662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu		
145 150 155		
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCC GGC		710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly		
160 165 170		
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC		758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His		
175 180 185 190		
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA		806
Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly		
195 200 205		

GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro 210 215 220	854
GTG TTT GTG GCC TAC TCG TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala 225 230 235	902
GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val 240 245 250	950
CCC AAC CTG GCG CTG GCC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro 255 260 265 270	998
GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg 275 280 285	1046
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser 290 295 300	1094
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg 305 310 315	1142
GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His 320 325 330	1190
CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly 335 340 345 350	1238
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His 355 360 365	1286
CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met 370 375 380	1334
AAG TAC CCC GTG TGG CCT CGC TAC AGT GCC TCT CTG CAG CCT GTG GTG Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val 385 390 395	1382
GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val 400 405 410	1430
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr 415 420 425 430	1478
GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val 435 440 445	1526
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu 450 455 460	1574
AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val 465 470 475	1622

ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met 480 485 490	1670
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu 495 500 505 510	1718
ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe 515 520 525	1766
G TG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val 530 535 540	1814
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met 545 550 555	1862
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe 560 565 570	1910
GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys 575 580 585 590	1958
AAG TCC GGG GGC CCA GCT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG Lys Ser Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu 595 600 605	2006
TGG GCG CTG GTC TTC AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC Trp Ala Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly 610 615 620	2054
ACC ACC AGC AAG ATC ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC Thr Thr Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile 625 630 635	2102
TTC CTC GCC AGA TAC ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG Phe Leu Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu 640 645 650	2150
CAA TAC ATC GAC ACT GTG TCG GGC CTC ACT GAC AAG AAG TTT CAG CGG Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg 655 660 665 670	2198
CCT CAA GAT CAG TAC CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly 675 680 685	2246
AGC ACG GAG CGG AAC ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His 690 695 700	2294
ATG GTC AAG TTC AAC CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC Met Val Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu 705 710 715	2342
AAG ATG GGG AAG CTG GAT GCC TTC ATC TAT GAT GCT GCT GTC CTC AAC Lys Met Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn 720 725 730	2390
TAC ATG GCA GGC AAG GAC GAG GGC TGC AAG CTG GTC ACC ATT GGG TCT Tyr Met Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser 735 740 745 750	2438

GGC AAG GTC TTT GCT ACC ACT GGC TAC GGC ATC GCC ATG CAG AAG GAC Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp 755 760 765	2486
TCC CAC TGG AAG CGG GCC ATA GAC CTG GCG CTC TTG CAG TTC CTG GGG Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly 770 775 780	2534
GAC GGA GAG ACA CAG AAA CTG GAG ACA GTG TGG CTC TCA GGG ATC TGC Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys 785 790 795	2582
CAG AAT GAG AAG AAC GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn 800 805 810	2630
ATG GCA GGC GTC TTC TAC ATG CTG CTG GTG GCC ATG GGG CTG GCC CTG Met Ala Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu 815 820 825 830	2678
CTG GTC TTC GCC TGG GAG CAC CTG GTC TAC TGG AAG CTG CGC CAC TCG Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser 835 840 845	2726
GTG CCC AAC TCA TCC CAG CTG GAC TTC CTG CTG GCT TTC AGC AGG GGC Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly 850 855 860	2774
ATC TAC AGC TGC TTC AGC GGG GTG CAG AGC CTC GCC AGC CCA CCG CGG Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg 865 870 875	2822
CAG GCC AGC CCG GAC CTC ACG GCC AGC TCG GCC CAG GCC AGC GTG CTC Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu 880 885 890	2870
AAG ATG CTG CAG GCA GCC CGC GAC ATG GTG ACC ACG GCG GGC GTA AGC Lys Met Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser 895 900 905 910	2918
AGC TCC CTG GAC CGC GCC ACT CGC ACC ATC GAG AAT TGG GGT GGC GGC Ser Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly 915 920 925	2966
CGC CGT CGC CCC CCA CCG TCC CCC TGC CCG ACC CCG CGG TCT GGC CCC Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro 930 935 940	3014
AGC CCA TGC CTG CCC ACC CCC GAC CGC CCC CCA GAG CCG AGC CCC ACG Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr 945 950 955	3062
GGC TGG GGA CCC CCA GAC GGG GGT CGC GCG GCC CTT GTG CGC AGG GCT Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala 960 965 970	3110
CCG CAG CCC CCG GGC CGC CCC CCG ACG CCG GGG CCG CCC CTG TCC GAC Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp 975 980 985 990	3158
GTC TCC CGA GTG TCG CGC CGC CCA GCC TGG GAG GCG CGG TGG CCG GTG Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val 995 1000 1005	3206
CGG ACC GGG CAC TGC GGG AGG CAC CTC TCG GCC TCC GAG CGG CCC CTG Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu 1010 1015 1020	3254

TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser 1025 1030 1035	3302
GCG CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC Gly Arg Pro Phe Leu Pro Leu Ph Pro Glu Pro Pro Glu Leu Glu Asp 1040 1045 1050	3350
CTG CCG CTG CTC GGT CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu 1055 1060 1065 1070	3398
CAC GCG GCC TGG GCC CGG GGC TCG CGC CCG CGT CAC GCT TCC CTG CCC His Ala Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro 1075 1080 1085	3446
AGC TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly 1090 1095 1100	3494
TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGA CAC TCG GCC TGC AGG Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg 1105 1110 1115	3542
CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala 1120 1125 1130	3590
TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG Cys Gln Glu Gly Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln 1135 1140 1145 1150	3638
CAC GTC TGC CTG CAC GCC CAC GCC CAC CTG CCA TTT TGC TGG GGG GCT His Val Cys Leu His Ala His Leu Pro Phe Cys Trp Gly Ala 1155 1160 1165	3686
GTC TGT CCT CAC CTT CCA CCC TGT GCC AGC CAC GGC TCC TGG CTC TCC Val Cys Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser 1170 1175 1180	3734
GGG GCC TGG GGG CCT CTG GGG CAC AGG GGC AGG ACT CTG GGG CTG GGC Gly Ala Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly 1185 1190 1195	3782
ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGG GTA GCC Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala 1200 1205 1210	3830
CGT GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser 1215 1220 1225 1230	3878
AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA Ser Leu Glu Ser Glu Val 1235	3926
GCTGGATTCT CTGCCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG GCTTTCTGG	3986
CTTCTACCAT GAAATCCTGG CCATGGGACC CCAGTGACAG ATGATGTCTT CCATGGTCAT	4046
CAGTGACCTC AGTAGCCCTCA AATCATGGTG AGGGCTGGGC TTTGCTGTC CTCTTCTCAC	4106
GCAGAGTTCT GCCAGGAGGG TGTGCTGTGG GGGTCAGACT CCTGAGGCTC TCCCTTCCT	4166
GGGGCTAGCC AGTTACTGGT CATGCCCTGCT CTGGGCATGG AGGCTGGAAC TTGTGGTTGA	4226

GGCAGGGCCA TCCCGATCCT TGCTCTACCT GGCTAGAGTT TCTTCTCATC AGAGCACTGG	4286
GACATTAAC CCACCTTTTC CCAGAAAAAA AAAAAAAAAA AAAG	4340

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1236 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly			
1	5	10	15
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val			
20	25	30	
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val			
35	40	45	
Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro			
50	55	60	
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln			
65	70	75	80
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu			
85	90	95	
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser			
100	105	110	
Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val			
115	120	125	
Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val			
130	135	140	
Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr			
145	150	155	160
Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala			
165	170	175	
Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser			
180	185	190	
Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro			
195	200	205	
Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe			
210	215	220	
Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala			
225	230	235	240
Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn			
245	250	255	
Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly			
260	265	270	

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
 275 280 285
 Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp
 290 295 300
 Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His
 305 310 315 320
 Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu
 325 330 335
 Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr
 340 345 350
 Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu
 355 360 365
 Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr
 370 375 380
 Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser
 385 390 395 400
 Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val
 405 410 415
 Glu Ser Pro Asp Pro Gly Thr Gly Cys Val Pro Asn Thr Val Pro
 420 425 430
 Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro
 435 440 445
 Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys
 450 455 460
 Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn
 465 470 475 480
 Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly
 485 490 495
 Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile
 500 505 510
 Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu
 515 520 525
 Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro
 530 535 540
 Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe
 545 550 555 560
 Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr
 565 570 575
 Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser
 580 585 590
 Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala
 595 600 605
 Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr
 610 615 620

Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu
 625 630 635 640
 Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr
 645 650 655
 Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln
 660 665 670
 Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr
 675 680 685
 Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val
 690 695 700
 Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met
 705 710 715 720
 Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met
 725 730 735
 Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys
 740 745 750
 Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His
 755 760 765
 Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly
 770 775 780
 Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn
 785 790 795 800
 Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala
 805 810 815
 Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val
 820 825 830
 Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro
 835 840 845
 Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr
 850 855 860
 Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala
 865 870 875 880
 Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Met
 885 890 895
 Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Ser Ser
 900 905 910
 Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly Arg Arg
 915 920 925
 Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro
 930 935 940
 Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp
 945 950 955 960
 Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln
 965 970 975

Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser
 980 985 990
 Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr
 995 1000 1005
 Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro
 1010 1015 1020
 Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg
 1025 1030 1035 1040
 Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro
 1045 1050 1055
 Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu His Ala
 1060 1065 1070
 Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro Ser Ser
 1075 1080 1085
 Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr
 1090 1095 1100
 Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu
 1105 1110 1115 1120
 Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln
 1125 1130 1135
 Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val
 1140 1145 1150
 Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala Val Cys
 1155 1160 1165
 Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser Gly Ala
 1170 1175 1180
 Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly Thr Gly
 1185 1190 1195 1200
 Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala Arg Gly
 1205 1210 1215
 Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu
 1220 1225 1230
 Glu Ser Glu Val
 1235

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

C TCT GAG GCT CAG CCT GTC CCC AG
 Ser Glu Ala Gln Pro Val Pro
 1 5

24

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Ala Gln Pro Val Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGAACGGGGT G

11

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4808 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 311..4705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCATGGGAC CGGGTGAGCG CTGAGAATCG CGGCCGCAGC CATCAGCCCT GGAGATGACC	60
AGGAGCGGCC ACTGCTGAGA ACTATGTGGA GAGAGGGCTGC GAGCCCTGCT GCAGAGCCTC	120
CGGCTGGGAT AGCCGCCCCC CGTGGGGCG ATGCGGACAG CGCGGGACAG CCAGGGAGC	180
GCGCTGGGCG CGCAGCATGC GGGAACCCGC TAAACCCGGT GGCTGCTGAG CGGGCCGAGA	240
TGCTCGTGCG CGCAGCGCGC CCCACTGCAT CCTCGACCTT CTCGGCTAC AGGGACCGTC	300

AGTGGCGACT ATG GGC AGA GTG GGC TAT TGG ACC CTG CTG GTG CTG CCG Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro 1 5 10	349
GCC CTT CTG GTC TGG CGC GGT CCG GCG CCG AGC GCG GCG GCG GAG AAG Ala Leu Leu Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys 15 20 25	397
GGT CCC CCC GCG CTA AAT ATT GCG GTG ATG CTG GGT CAC AGC CAC GAC Gly Pro Pro Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp 30 35 40 45	445
GTC ACA GAG CGC GAA CTT CGA ACA CTG TGG GGC CCC GAG CAG GCG GCG Val Thr Glu Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala 50 55 60	493
GGG CTG CCC CTG GAC GTG AAC GTG GTA GCT CTG CTG ATG AAC CGC ACC Gly Leu Pro Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr 65 70 75	541
GAC CCC AAG AGC CTC ATC ACG CAC GTG TGC GAC CTC ATG TCC GGG GCA Asp Pro Lys Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala 80 85 90	589
CGC ATC CAC GGC CTC GTG TTT GGG GAC GAC ACG GAC CAG GAG GCC GTA Arg Ile His Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val 95 100 105	637
GCC CAG ATG CTG GAT TTT ATC TCC TCC CAC ACC TTC GTC CCC ATC TTG Ala Gln Met Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu 110 115 120 125	685
GCC ATT CAT GGG GGC GCA TCT ATG ATC ATG GCT GAC AAG GAT CCG ACG Gly Ile His Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr 130 135 140	733
TCT ACC TTC TTC CAG TTT GGA GCG TCC ATC CAG CAG CAA GCC ACG GTC Ser Thr Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val 145 150 155	781
ATG CTG AAG ATC ATG CAG GAT TAT GAC TGG CAT GTC TTC TCC CTG GTG Met Leu Lys Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val 160 165 170	829
ACC ACT ATC TTC CCT GGC TAC AGG GAA TTC ATC AGC TTC GTC AAG ACC Thr Thr Ile Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr 175 180 185	877
ACA GTG GAC AAC AGC TTT GTG GGC TGG GAC ATG CAG AAT GTG ATC ACA Thr Val Asp Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr 190 195 200 205	925
CTG GAC ACT TCC TTT GAG GAT GCA AAG ACA CAA GTC CAG CTG AAG AAG Leu Asp Thr Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys 210 215 220	973
ATC CAC TCT TCT GTC ATC TTG CTC TAC TGT TCC AAA GAC GAG GCT GTT Ile His Ser Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val 225 230 235	1021
CTC ATT CTG AGT GAG GCC CGC TCC CTT GGC CTC ACC GGG TAT GAT TTC Leu Ile Leu Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe 240 245 250	1069
TTC TGG ATT GTC CCC AGC TTG GTC TCT GGG AAC ACG GAG CTC ATC CCA Phe Trp Ile Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro 255 260 265	1117

AAA GAG TTT CCA TCG GGA CTC ATT TCT GTC TCC TAC GAT GAC TGG GAC Lys Glu Phe Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp 270 275 280 285	1165
TAC AGC CTG GAG GCG AGA GTG AGG GAC GGC ATT GGC ATC CTA ACC ACC Tyr Ser Leu Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr 290 295 300 305	1213
GCT GCA TCT TCT ATG CTG GAG AAG TTC TCC TAC ATC CCC GAG GCC AAG Ala Ala Ser Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys 305 310 315 320	1261
GCC AGC TGC TAC GGG CAG ATG GAG AGG CCA GAG GTC CCG ATG CAC ACC Ala Ser Cys Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr 320 325 330 335	1309
TTG CAC CCA TTT ATG GTC AAT GTT ACA TGG GAT GGC AAA GAC TTA TCC Leu His Pro Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser 335 340 345 350	1357
TTC ACT GAG GAA GGC TAC CAG GTG CAC CCC AGG CTG GTG GTG ATT GTG Phe Thr Glu Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val 350 355 360 365	1405
CTG AAC AAA GAC CGG GAA TGG GAA AAG GTG GGC AAG TGG GAG AAC CAT Leu Asn Lys Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His 370 375 380 385	1453
ACG CTG AGC CTG AGG CAC GCC GTG TGG CCC AGG TAC AAG TCC TTC TCC Thr Leu Ser Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser 385 390 395 400	1501
GAC TGT GAG CCG GAT GAC AAC CAT CTC AGC ATC GTC ACC CTG GAG GAG Asp Cys Glu Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu 400 405 410 415	1549
GCC CCA TTC GTC ATC GTG GAA GAC ATA GAC CCC CTG ACC GAG ACG TGT Ala Pro Phe Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys 415 420 425 430	1597
GTG AGG AAC ACC GTG CCA TGT CCG AAG TTC GTC AAA ATC AAC AAT TCA Val Arg Asn Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser 430 435 440 445	1645
ACC AAT GAG GGG ATG AAT GTG AAG AAA TGC TGC AAG GGG TTC TGC ATT Thr Asn Glu Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile 450 455 460 465	1693
GAT ATT CTG AAG AAG CTT TCC AGA ACT GTG AAG TTT ACT TAC GAC CTC Asp Ile Leu Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu 465 470 475 480	1741
TAT CTG GTG ACC AAT GGG AAG CAT GGC AAG AAA GTT AAC AAT GTG TGG Tyr Leu Val Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp 480 485 490 495	1789
AAT GGA ATG ATC GGT GAA GTG GTC TAT CAA CGG GCA GTC ATG GCA GTT Asn Gly Met Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val 495 500 505 510	1837
GGC TCG CTC ACC ATC AAT GAG GAA CGT TCT GAA GTG GTG GAC TTC TCT Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser 510 515 520 525	1885
GTG CCC TTT GTG GAA ACG GGA ATC AGT GTC ATG GTT TCA AGA AGT AAT Val Pro Phe Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn 530 535 540 545	1933

GGC ACC GTC TCA CCT TCT GCT TTT CTA GAA CCA TTC AGC GCC TCT GTC Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val 545 550 555	1981
TGG GTG ATG ATG TTT GTG ATG CTG CTC ATT GTT TCT GCC ATA GCT GTT Trp Val Met Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val 560 565 570	2029
TGG GTC TTG GAT TAC TCC AGC CCT GTT GGA TAC AAC AGA AAC TTA GCC Trp Val Leu Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala 575 580 585	2077
AAA GGG AAA GCA CCC CAT GGG CCT TCT TTT ACA ATT GGA AAA GCT ATA Lys Gly Lys Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile 590 595 600 605	2125
TGG CTT CTT TGG GGC CTG GTG TTC AAT AAC TCC GTG CCT GTC CAG AAT Trp Leu Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn 610 615 620	2173
CCT AAA GGG ACC ACC AGC AAG ATC ATG GTA TCT GTA TGG GCC TTC TTC Pro Lys Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe 625 630 635	2221
GCT GTC ATA TTC CTG GCT AGC TAC ACA GCC AAT CTG GCT GCC TTC ATG Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met 640 645 650	2269
ATC CAA GAG GAA TTT GTG GAC CAA GTG ACC GGC CTC AGT GAC AAA AAG Ile Gln Glu Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys 655 660 665	2317
TTT CAG AGA CCT CAT GAC TAT TCC CCA CCT TTT CGA TTT GGG ACA GTG Phe Gln Arg Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val 670 675 680 685	2365
CCT AAT GGA AGC ACG GAG AGA AAC ATT CGG AAT AAC TAT CCC TAC ATG Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met 690 695 700	2413
CAT CAG TAC ATG ACC AAA TTT AAT CAG AAA GGA GTA GAG GAC GCC TTG His Gln Tyr Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu 705 710 715	2461
GTC AGC CTG AAA ACG GGG AAG CTG GAC GCT TTC ATC TAC GAT GCC GCA Val Ser Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala 720 725 730	2509
GTC TTG AAT TAC AAG GCT GGG AGG GAT GAA GGC TGC AAG CTG GTG ACC Val Leu Asn Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr 735 740 745	2557
ATC GGG AGT GGG TAC ATC TTT GCC ACC ACC GGT TAT GGA ATT GCC CTT Ile Gly Ser Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu 750 755 760 765	2605
CAG AAA GGC TCT CCT TGG AAG AGG CAG ATC GAC CTG GCC TTG CTT CAG Gln Lys Gly Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Gln 770 775 780	2653
TTT GTG GGT GAT GGT GAG ATG GAG GAG CTG GAG ACC CTG TGG CTC ACT Phe Val Gly Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr 785 790 795	2701
GGG ATC TGC CAC AAC GAG AAG AAC GAC GTG ATG AGC AGC CAG CTG GAC Gly Ile Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp 800 805 810	2749

ATT GAC AAC ATG GCG GGC GTA TTC TAC ATG CTG GCT GCC GCC ATG GCC Ile Asp Asn Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala 815	820	825	2797
CTT AGC CTC ATC ACC TTC ATC TGG GAG CAC CTC TTC TAC TGG AAG CTG Leu Ser Leu Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu 830	835	840	845
CGC TTC TGT TTC ACG GGC GTG TGC TCC GAC CGG CCT GGG TTG CTC TTC Arg Phe Cys Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe 850	855	860	2893
TCC ATC AGC AGG GGC ATC TAC AGC TGC ATT CAT GGA GTG CAC ATT GAA Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu 865	870	875	2941
GAA AAG AAG AAG TCT CCA GAC TTC AAT CTG ACG GGA TCC CAG AGC AAC Glu Lys Lys Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn 880	885	890	2989
ATG TTA AAA CTC CTC CGG TCA GCC AAA AAC ATT TCC AGC ATG TCC AAC Met Leu Lys Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn 895	900	905	3037
ATG AAC TCC TCA AGA ATG GAC TCA CCC AAA AGA GCT GCT GAC TTC ATC Met Asn Ser Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile 910	915	920	925
CAA AGA GGT TCC CTC ATC ATG GAC ATG GTT TCA GAT AAG GGG AAT TTG Gln Arg Gly Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu 930	935	940	3133
ATG TAC TCA GAC AAC AGG TCC TTT CAG GGG AAA GAG AGC ATT TTT GGA Met Tyr Ser Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly 945	950	955	3181
GAC AAC ATG AAC GAA CTC CAA ACA TTT GTG GCC AAC CGG CAG AAG GAT Asp Asn Met Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp 960	965	970	3229
AAC CTC AAT AAC TAT GTA TTC CAG GGA CAA CAT CCT CTT ACT CTC AAT Asn Leu Asn Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn 975	980	985	3277
GAG TCC AAC CCT AAC ACG GTG GAG GTG GCC GTG AGC ACA GAA TCC AAA Glu Ser Asn Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys 990	995	1000	1005
GCG AAC TCT AGA CCC CGG CAG CTG TGG AAG AAA TCC GTG GAT TCC ATA Ala Asn Ser Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile 1010	1015	1020	3373
CGC CAG GAT TCA CTA TCC CAG AAT CCA GTC TCC CAG AGG GAT GAG GCA Arg Gln Asp Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala 1025	1030	1035	3421
ACA GCA GAG AAT AGG ACC CAC TCC CTA AAG AGC CCT AGG TAT CTT CCA Thr Ala Glu Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro 1040	1045	1050	3469
GAA GAG ATG GCC CAC TCT GAC ATT TCA GAA ACG TCA AAT CGG GCC ACG Glu Glu Met Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr 1055	1060	1065	3517
TGC CAC AGG GAA CCT GAC AAC ACT AAG AAC CAC AAA ACC AAG GAC AAC Cys His Arg Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn 1070	1075	1080	3565
		1085	

TTT AAA AGG TCA GTG GCC TCC AAA TAC CCC AAG GAC TGT AGT GAG GTC Phe Lys Arg Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val 1090 1095 1100	3613
GAG CGC ACC TAC CTG AAA ACC AAA TCA AGC TCC CCT AGA GAC AAG ATC Glu Arg Thr Tyr Leu Lys Thr Lys Ser Ser Pro Arg Asp Lys Ile 1105 1110 1115	3661
TAC ACT ATA GAT GGT GAG AAG GAG CCT CGT TTC CAC TTA GAT CCA CCC Tyr Thr Ile Asp Gly Glu Lys Pro Gly Phe His Leu Asp Pro Pro 1120 1125 1130	3709
CAG TTT GTT GAA AAT GTG ACC CTG CCC GAG AAC GTG GAC TTC CCG GAC Gln Phe Val Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp 1135 1140 1145	3757
CCC TAC CAG GAT CCC AGT GAA AAC TTC CGC AAG GGG GAC TCC ACG CTG Pro Tyr Gln Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu 1150 1155 1160 1165	3805
CCA ATG AAC CGG AAC CCC TTG CAT AAT GAA GAG GGG CTT TCC AAC AAC Pro Met Asn Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn ~1170 1175 1180	3853
GAC CAG TAT AAA CTC TAC TCC AAG CAC TTC ACC TTG AAA GAC AAG GGT Asp Gln Tyr Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly 1185 1190 1195	3901
TCC CCG CAC AGT GAG ACC AGC GAG CGA TAC CGG CAG AAC TCC ACG CAC Ser Pro His Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His 1200 1205 1210	3949
TGC AGA AGC TGC CTT TCC AAC ATG CCC ACC TAT TCA GGC CAC TTC ACC Cys Arg Ser Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr 1215 1220 1225	3997
ATG AGG TCC CCC TTC AAG TGC GAT GCC TGC CTG CGG ATG GGG AAC CTC Met Arg Ser Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu 1230 1235 1240 1245	4045
TAT GAC ATC GAT GAA GAC CAG ATG CTT CAG GAG ACA GGT AAC CCA GCC Tyr Asp Ile Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala 1250 1255 1260	4093
ACC GGG GAG CAG GTC TAC CAG CAG GAC TGG GCA CAG AAC AAT GCC CTT Thr Gly Glu Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu 1265 1270 1275	4141
CAA TTA CAA AAG AAC AAG CTA AGG ATT AGC CGT CAG CAT TCC TAC GAT Gln Leu Gln Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp 1280 1285 1290	4189
AAC ATT GTC GAC AAA CCT AGG GAG CTA GAC CTT AGC AGG CCC TCC CGG Asn Ile Val Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg 1295 1300 1305	4237
AGC ATA AGC CTC AAG GAC AGG GAA CGG CTT CTG GAG GGA AAT TTT TAC Ser Ile Ser Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr 1310 1315 1320 1325	4285
GGC AGC CTG TTT AGT GTC CCC TCA AGC AAA CTC TCG GGG AAA AAA AGC Gly Ser Leu Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser 1330 1335 1340	4333
TCC CTT TTC CCC CAA GGT CTG GAG GAC AGC AAG AGG AGC AAG TCT CTC Ser Leu Phe Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu 1345 1350 1355	4381

TTG CCA GAC CAC ACC TCC GAT AAC CCT TTC CTC CAC TCC CAC AGG GAT Leu Pro Asp His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp 1360 1365 1370	4429
GAC CAA CGC TTG GTT ATT GGG AGA TGC CCC TCG GAC CCT TAC AAA CAC Asp Gln Arg Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His 1375 1380 1385	4477
TCG TTG CCA TCC CAG GCG GTG AAT GAC AGC TAT CTT CGG TCG TCC TTG Ser Leu Pro Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu 1390 1395 1400 1405	4525
AGG TCA ACG GCA TCG TAC TGT TCC AGG GAC AGT CGG GGC CAC AAT GAT Arg Ser Thr Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp 1410 1415 1420	4573
GTG TAT ATT TCG GAG CAT GTT ATG CCT TAT GCT GCA AAT AAG AAT AAT Val Tyr Ile Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn 1425 1430 1435	4621
ATG TAC TCT ACC CCC AGG GTT TTA AAT TCC TGC AGC AAT AGA CGC GTG Met Tyr Ser Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val 1440 1445 1450	4669
TAC AAG GAA ATG CCT AGT ATC GAA TCT GAT GTT TAAAAATCTT CCATTAATGT Tyr Lys Glu Met Pro Ser Ile Glu Ser Asp Val 1455 1460 146	4722
TTTATCTATA GGGAAATACA CGTAATGGCC AATGTTCTGG AGGGTAAATG TTGGATGTCC	4782
AATAGTGCCC TGCTAAGAGG AAGGAG	4808

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1464 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu 1 5 10 15
Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro 20 25 30
Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp Val Thr Glu 35 40 45
Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala Gly Leu Pro 50 55 60
Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr Asp Pro Lys 65 70 75 80
Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala Arg Ile His 85 90 95
Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val Ala Gln Met 100 105 110
Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu Gly Ile His 115 120 125

Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr Ser Thr Phe
 130 135 140
 Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val Met Leu Lys
 145 150 155 160
 Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val Thr Thr Ile
 165 170 175
 Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr Thr Val Asp
 180 185 190
 Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr Leu Asp Thr
 195 200 205
 Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys Ile His Ser
 210 215 220
 Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val Leu Ile Leu
 225 230 235 240
 Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe Phe Trp Ile
 245 250 255
 Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro Lys Glu Phe
 260 265 270
 Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp Tyr Ser Leu
 275 285
 Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr Ala Ala Ser
 290 295 300
 Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys Ala Ser Cys
 305 310 315 320
 Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr Leu His Pro
 325 330 335
 Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser Phe Thr Glu
 340 345 350
 Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val Leu Asn Lys
 355 360 365
 Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His Thr Leu Ser
 370 375 380
 Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser Asp Cys Glu
 385 390 395 400
 Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe
 405 410 415
 Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys Val Arg Asn
 420 425 430
 Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser Thr Asn Glu
 435 440 445
 Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu
 450 455 460
 Lys Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu Tyr Leu Val
 465 470 475 480

Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp Asn Gly Met
 485 490 495
 Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val Gly Ser Leu
 500 505 510
 Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro Phe
 515 520 525
 Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr Val
 530 535 540
 Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val Trp Val Met
 545 550 555 560
 Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val Trp Val Leu
 565 570 575
 Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala Lys Gly Lys
 580 585 590
 Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu
 595 600 605
 Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly
 610 615 620
 Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val Ile
 625 630 635 640
 Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu
 645 650 655
 Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys Phe Gln Arg
 660 665 670
 Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly
 675 680 685
 Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met His Gln Tyr
 690 695 700
 Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu Val Ser Leu
 705 710 715 720
 Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn
 725 730 735
 Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser
 740 745 750
 Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu Gln Lys Gly
 755 760 765
 Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln Phe Val Gly
 770 775 780
 Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr Gly Ile Cys
 785 790 795 800
 His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp Asn
 805 810 815
 Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala Leu Ser Leu
 820 825 830

Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu Arg Phe Cys
 835 840 845
 Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe Ser Ile Ser
 850 855 860
 Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu Glu Lys Lys
 865 870 875 880
 Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn Met Leu Lys
 885 890 895
 Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn Met Asn Ser
 900 905 910
 Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile Gln Arg Gly
 915 920 925
 Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu Met Tyr Ser
 930 935 940
 Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly Asp Asn Met
 945 950 955 960
 Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp Asn Leu Asn
 965 970 975
 Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn Glu Ser Asn
 980 985 990
 Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys Ala Asn Ser
 995 1000 1005
 Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile Arg Gln Asp
 1010 1015 1020
 Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala Thr Ala Glu
 1025 1030 1035 1040
 Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro Glu Glu Met
 1045 1050 1055
 Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr Cys His Arg
 1060 1065 1070
 Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn Phe Lys Arg
 1075 1080 1085
 Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val Glu Arg Thr
 1090 1095 1100
 Tyr Leu Lys Thr Lys Ser Ser Pro Arg Asp Lys Ile Tyr Thr Ile
 1105 1110 1115 1120
 Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro Gln Phe Val
 1125 1130 1135
 Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp Pro Tyr Gln
 1140 1145 1150
 Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu Pro Met Asn
 1155 1160 1165
 Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn Asp Gln Tyr
 1170 1175 1180

Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly Ser Pro His
 1185 1190 1195 1200
 Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His Cys Arg Ser
 1205 1210 1215
 Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr Met Arg Ser
 1220 1225 1230
 Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu Tyr Asp Ile
 1235 1240 1245
 Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala Thr Gly Glu
 1250 1255 1260
 Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Ala Leu Gln Leu Gln
 1265 1270 1275 1280
 Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp Asn Ile Val
 1285 1290 1295
 Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg Ser Ile Ser
 1300 1305 1310
 Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr Gly Ser Leu
 1315 1320 1325
 Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser Ser Leu Phe
 1330 1335 1340
 Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu Leu Pro Asp
 1345 1350 1355 1360
 His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp Asp Gln Arg
 1365 1370 1375
 Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro
 1380 1385 1390
 Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr
 1395 1400 1405
 Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile
 1410 1415 1420
 Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser
 1425 1430 1435 1440
 Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Glu
 1445 1450 1455
 Met Pro Ser Ile Glu Ser Asp Val
 1460

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGGGAGGC GGCGGCGCG GACTCTCTTC CGGGCGCAG CGCCCTTCC CCCTCGGACC	60
CTCCGGTGGAA CATG	74

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 210..4664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTGAATTGTC ATCTCTTCAA GACACAAGAT TAAAACAAAA TTTACGCTAA ATTGGATTTC	60
AAATTATCTT CCGTTCATTT ATCCTTCGTC TTTCTTATGT GGATATGCAA GCGAGAAGAA	120
GGGACTGGAC ATTCCCAACA TGCTCACTCC CTTAACATGTG CCGTCTAGAG GTTTGGCTTC	180
TACAAACCAA GGGAGTCGAC GAGTTGAAG ATG AAG CCC AGA GCG GAG TGC TGT	233
Met Lys Pro Arg Ala Glu Cys Cys	
1 5	
TCT CCC AAG TTC TGG TTG GTG TTG GCC GTC CTG GCC GTG TCA GGC AGC	281
Ser Pro Lys Phe Trp Leu Val Leu Ala Val Leu Ala Val Ser Gly Ser	
10 15 20	
AGA GCT CGT TCT CAG AAG AGC CCC CCC AGC ATT GGC ATT GCT GTC ATC	329
Arg Ala Arg Ser Gln Lys Ser Pro Pro Ser Ile Gly Ile Ala Val Ile	
25 30 35 40	
CTC GTG GGC ACT TCC GAC GAG GTG GCC ATC AAG GAT GCC CAC GAG AAA	377
Leu Val Gly Thr Ser Asp Glu Val Ala Ile Lys Asp Ala His Glu Lys	
45 50 55	
GAT GAT TTC CAC CAT CTC TCC GTG GTA CCC CGG GTG GAA CTG GTA GCC	425
Asp Asp Phe His His Leu Ser Val Val Pro Arg Val Glu Leu Val Ala	
60 65 70	
ATG AAT GAG ACC GAC CCA AAG AGC ATC ATC ACC CGC ATC TGT GAT CTC	473
Met Asn Glu Thr Asp Pro Lys Ser Ile Ile Thr Arg Ile Cys Asp Leu	
75 80 85	
ATG TCT GAC CGG AAG ATC CAG GGG GTG GTG TTT GCT GAT GAC ACA GAC	521
Met Ser Asp Arg Lys Ile Gln Gly Val Val Phe Ala Asp Asp Thr Asp	
90 95 100	
CAG GAA GCC ATC GCC CAG ATC CTC GAT TTC ATT TCA GCA CAG ACT CTC	569
Gln Glu Ala Ile Ala Gln Ile Leu Asp Phe Ile Ser Ala Gln Thr Leu	
105 110 115 120	
ACC CCG ATC CTG GGC ATC CAC GGG GGC TCC TCT ATG ATA ATG GCA GAT	617
Thr Pro Ile Leu Gly Ile His Gly Gly Ser Ser Met Ile Met Ala Asp	
125 130 135	

AAG GAT GAA TCC TCC ATG TTC CAG TTT GGC CCA TCA ATT GAA CAG Lys Asp Glu Ser Ser Met Phe Phe Gln Phe Gly Pro Ser Ile Glu Gln 140 145 150	665
CAA GCT TCC GTA ATG CTC AAC ATC ATG GAA GAA TAT GAC TGG TAC ATC Gln Ala Ser Val Met Leu Asn Ile Met Glu Glu Tyr Asp Trp Tyr Ile 155 160 165	713
TTC TCT ATC GTC ACC ACC TAT TTC CCT GGC TAC CAG GAC TTT GTA AAC Phe Ser Ile Val Thr Thr Tyr Phe Pro Gly Tyr Gln Asp Phe Val Asn 170 175 180	761
AAG ATC CGC AGC ACC ATT GAG AAT AGC TTT GTG GGC TGG GAG CTA GAG Lys Ile Arg Ser Thr Ile Glu Asn Ser Phe Val Gly Trp Glu Leu Glu 185 190 195 200	809
GAG GTC CTC CTA CTG GAC ATG TCC CTG GAC GAT GGA GAT TCT AAG ATC Glu Val Leu Leu Asp Met Ser Leu Asp Asp Gly Asp Ser Lys Ile 205 210 215	857
CAG AAT CAG CTC AAG AAA CTT CAA AGC CCC ATC ATT CTT CTT TAC TGT Gln Asn Gln Leu Lys Lys Leu Gln Ser Pro Ile Ile Leu Leu Tyr Cys 220 225 230	905
ACC AAG GAA GAA GCC ACC TAC ATC TTT GAA GTG GCC AAC TCA GTA GGG Thr Lys Glu Glu Ala Thr Tyr Ile Phe Glu Val Ala Asn Ser Val Gly 235 240 245	953
CTG ACT GGC TAT GGC TAC ACG TGG ATC GTG CCC AGT CTG GTG GCA GGG Leu Thr Gly Tyr Gly Tyr Thr Trp Ile Val Pro Ser Leu Val Ala Gly 250 255 260	1001
GAT ACA GAC ACA GTG CCT GCG GAG TTC CCC ACT GGG CTC ATC TCT GTA Asp Thr Asp Thr Val Pro Ala Glu Phe Pro Thr Gly Leu Ile Ser Val 265 270 275 280	1049
TCA TAT GAT GAA TGG GAC TAT GGC CTC CCC CCC AGA GTG AGA GAT GGA Ser Tyr Asp Glu Trp Asp Tyr Gly Leu Pro Pro Arg Val Arg Asp Gly 285 290 295	1097
ATT GCC ATA ATC ACC ACT GCT GCT TCT GAC ATG CTG TCT GAG CAC AGC Ile Ala Ile Ile Thr Thr Ala Ala Ser Asp Met Leu Ser Glu His Ser 300 305 310	1145
TTC ATC CCT GAG CCC AAA AGC AGT TGT TAC AAC ACC CAC GAG AAG AGA Phe Ile Pro Glu Pro Lys Ser Ser Cys Tyr Asn Thr His Glu Lys Arg 315 320 325	1193
ATC TAC CAG TCC AAT ATG CTA AAT AGG TAT CTG ATC AAT GTC ACT TTT Ile Tyr Gln Ser Asn Met Leu Asn Arg Tyr Leu Ile Asn Val Thr Phe 330 335 340	1241
GAG GGG AGG AAT TTG TCC TTC AGT GAA GAT GGC TAC CAG ATG CAC CCG Glu Gly Arg Asn Leu Ser Phe Ser Glu Asp Gly Tyr Gln Met His Pro 345 350 355 360	1289
AAA CTG GTG ATA ATT CTT CTG AAC AAG GAG AGG AAG TGG GAA AGG GTG Lys Leu Val Ile Leu Leu Asn Lys Glu Arg Lys Trp Glu Arg Val 365 370 375	1337
GGG AAG TGG AAA GAC AAG TCC CTG CAG ATG AAG TAC TAT GTG TGG CCC Gly Lys Trp Lys Asp Lys Ser Leu Gln Met Lys Tyr Tyr Val Trp Pro 380 385 390	1385
CGA ATG TGT CCA GAG ACT GAA GAG CAG GAG GAT GAC CAT CTG AGC ATT Arg Met Cys Pro Glu Thr Glu Glu Gln Glu Asp Asp His Leu Ser Ile 395 400 405	1433

GTG ACC CTG GAG GAG CCA CCA TTT GTC ATT GTG GAA AGT GTG GAC CCT Val Thr Leu Glu Glu Ala Pro Phe Val Ile Val Glu Ser Val Asp Pro 410 415 420	1481
CTG AGT GGA ACC TGC ATG AGG AAC ACA GTC CCC TGC CAA AAA CGC ATA Leu Ser Gly Thr Cys Met Arg Asn Thr Val Pro Cys Gln Lys Arg Ile 425 430 435 440	1529
GTC ACT GAG AAT AAA ACA GAC GAG GAG CCG GGT TAC ATC AAA AAA TGC Val Thr Glu Asn Lys Thr Asp Glu Glu Pro Gly Tyr Ile Lys Lys Cys 445 450 455	1577
TGC AAG GGG TTC TGT ATT GAC ATC CTT AAG AAA ATT TCT AAA TCT GTG Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys Ile Ser Lys Ser Val 460 465 470	1625
AAG TTC ACC TAT GAC CTT TAC CTG GTT ACC AAT GGC AAG CAT GGG AAG Lys Phe Thr Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys 475 480 485	1673
AAA ATC AAT GGA ACC TGG AAT GGT ATG ATT GGA GAG GTG GTC ATG AAG Lys Ile Asn Gly Thr Trp Asn Gly Met Ile Gly Glu Val Val Met Lys 490 495 500	1721
AGG GCC TAC ATC GCA GTG GGC TCA CTC ACC ATC AAT GAG GAA CGA TCG Arg Ala Tyr Met Ala Val Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser 505 510 515 520	1769
GAG GTG GTC GAC TTC TCT GTG CCC TTC ATA GAG ACA GGC ATC AGT GTC Glu Val Val Asp Phe Ser Val Pro Phe Ile Glu Thr Gly Ile Ser Val 525 530 535	1817
ATG GTG TCA CGC AGC AAT GGG ACT GTC TCA CCT TCT GCC TTC TTA GAG Met Val Ser Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu 540 545 550	1865
CCA TTC AGC GCT GAC GTA TGG GTG ATG ATG TTT GTG ATG CTG CTC ATC Pro Phe Ser Ala Asp Val Trp Val Met Met Phe Val Met Leu Leu Ile 555 560 565	1913
GTC TCA GCC GTG GCT GTC TTT GTC TTT GAG TAC TTC AGC CCT GTG GGT Val Ser Ala Val Ala Val Phe Val Phe Glu Tyr Phe Ser Pro Val Gly 570 575 580	1961
TAT AAC AGG TGC CTC GCT GAT GGC AGA GAG CCT GGT GGA CCC TCT TTC Tyr Asn Arg Cys Leu Ala Asp Gly Arg Glu Pro Gly Pro Ser Phe 585 590 595 600	2009
ACC ATC GGC AAA GCT ATT TGG TTG CTC TGG GGT CTG GTG TTT AAC AAC Thr Ile Gly Lys Ala Ile Trp Leu Leu Trp Gly Leu Val Phe Asn Asn 605 610 615	2057
TCC GTA CCT GTG CAG AAC CCA AAG GGG ACC ACC TCC AAG ATC ATG GTG Ser Val Pro Val Gln Asn Pro Lys Gly Thr Thr Ser Lys Ile Met Val 620 625 630	2105
TCA GTG TGG GCC TTC TTT GCT GTC ATC TTC CTG GCC AGC TAC ACT GCC Ser Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala 635 640 645	2153
AAC TTA GCT GCC TTC ATG ATC CAA GAG GAA TAT GTG GAC CAG GTT TCT Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp Gln Val Ser 650 655 660	2201
GGC CTG AGC GAC AAA AAG TTC CAG AGA CCT AAT GAC TTC TCA CCC CCT Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Asn Asp Phe Ser Pro Pro 665 670 675 680	2249

TTC CGC TTT GGG ACC GTG CCC AAC GGC AGC ACA GAG AGA AAT ATT CGC Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg 685	690	695	2297
AAT AAC TAT GCA GAA ATG CAT GCC TAC ATG GGA AAG TTC AAC CAG AGG Asn Asn Tyr Ala Glu Met His Ala Tyr Met Gly Lys Phe Asn Gln Arg 700	705	710	2345
GGT GTA GAT GAT GCA TTG CTC TCC CTG AAA ACA GGG AAA CTG GAT GCC Gly Val Asp Asp Ala Leu Leu Ser Leu Lys Thr Gly Lys Leu Asp Ala 715	720	725	2393
TTC ATC TAT GAT GCA GCA GTG CTG AAC TAT ATG GCA GGC AGA GAT GAA Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Arg Asp Glu 730	735	740	2441
GGC TGC AAG CTG GTG ACC ATT GGC AGT GGG AAG GTC TTT GCT TCC ACT Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Ser Thr 745	750	755	2489
GGC TAT GGC ATT GCC ATC CAA AAA GAT TCT GGG TGG AAG CGC CAG GTG Gly Tyr Gly Ile Ile Gln Lys Asp Ser Gly Trp Lys Arg Gln Val 765	770	775	2537
GAC CTT GCT ATC CTG CAG CTC TTT GGA GAT GGG GAG ATG GAA GAA CTG Asp Leu Ala Ile Leu Gln Leu Phe Gly Asp Gly Glu Met Glu Glu Leu 780	785	790	2585
GAA GCT CTC TGG CTC ACT GGC ATT TGT CAC AAT GAG AAG AAT GAG GTC Glu Ala Leu Trp Leu Thr Gly Ile Cys His Asn Glu Lys Asn Glu Val 795	800	805	2633
ATG AGC AGC CAG CTG GAC ATT GAC AAC ATG GCA GGG GTC TTC TAC ATG Met Ser Ser Gln Leu Asp Ile Asp Asn Met Ala Gly Val Phe Tyr Met 810	815	820	2681
TTG GGG GCG GCC ATG GCT CTC AGC CTC ATC ACC TTC ATC TGC GAA CAC Leu Gly Ala Ala Met Ala Leu Ser Leu Ile Thr Phe Ile Cys Glu His 825	830	835	2729
CTT TTC TAT TGG CAG TTC CGA CAT TGC TTT ATG GGT GTC TGT TCT GGC Leu Phe Tyr Trp Gln Phe Arg His Cys Phe Met Gly Val Cys Ser Gly 845	850	855	2777
AAG CCT GGC ATG GTC TTC TCC ATC AGC AGA GGT ATC TAC AGC TGC ATC Lys Pro Gly Met Val Phe Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile 860	865	870	2825
CAT GGG GTG GCG ATC GAG GAG CGC CAG TCT GTA ATG AAC TCC CCC ACC His Gly Val Ala Ile Glu Glu Arg Gln Ser Val Met Asn Ser Pro Thr 875	880	885	2873
GCA ACC ATG AAC AAC ACA CAC TCC AAC ATC CTG CGC CTG CTG CGC ACG Ala Thr Met Asn Asn Thr His Ser Asn Ile Leu Arg Leu Leu Arg Thr 890	895	900	2921
GCC AAG AAC ATG GCT AAC CTG TCT GGT GTG AAT GGC TCA CCG CAG AGC Ala Lys Asn Met Ala Asn Leu Ser Gly Val Asn Gly Ser Pro Gln Ser 905	910	915	2969
GCC CTG GAC TTC ATC CGA CGG GAG TCA TCC GTC TAT GAC ATC TCA GAG Ala Leu Asp Phe Ile Arg Arg Glu Ser Ser Val Tyr Asp Ile Ser Glu 925	930	935	3017
CAC CGC CGC AGC TTC ACG CAT TCT GAC TGC AAA TCC TAC AAC AAC CCG His Arg Arg Ser Phe Thr His Ser Asp Cys Lys Ser Tyr Asn Asn Pro 940	945	950	3065

CCC TGT GAG GAG AAC CTC TTC AGT GAC TAC ATC AGT GAG GTA GAG AGA Pro Cys Glu Glu Asn Leu Phe Ser Asp Tyr Ile Ser Glu Val Glu Arg 955 960 965	3113
ACG TTC GGG AAC CTG CAG CTG AAG GAC AGC AAC GTG TAC CAA GAT CAC Thr Phe Gly Asn Leu Gln Leu Lys Asp Ser Asn Val Tyr Gln Asp His 970 975 980	3161
TAC CAC CAT CAC CAC CGG CCC CAT AGT ATT GGC AGT GCC AGC TCC ATC Tyr His His His Arg Pro His Ser Ile Gly Ser Ala Ser Ser Ile 985 990 995 1000	3209
GAT GGG CTC TAC GAC TGT GAC AAC CCA CCC TTC ACC ACC CAG TCC AGG Asp Gly Leu Tyr Asp Cys Asp Asn Pro Pro Phe Thr Thr Gln Ser Arg 1005 1010 1015	3257
TCC ATC AGC AAG AAG CCC CTG GAC ATC GGC CTC CCC TCC TCC AAG CAC Ser Ile Ser Lys Lys Pro Leu Asp Ile Gly Leu Pro Ser Ser Lys His 1020 1025 1030	3305
AGC CAG CTC AGT GAC CTG TAC GGC AAA TTC TCC TTC AAG AGC GAC CGC Ser Gln Leu Ser Asp Leu Tyr Gly Lys Phe Ser Phe Lys Ser Asp Arg 1035 1040 1045	3353
TAC AGT GGC CAC GAC GAC TTG ATC CGC TCC GAT GTC TCT GAC ATC TCA Tyr Ser Gly His Asp Asp Leu Ile Arg Ser Asp Val Ser Asp Ile Ser 1050 1055 1060	3401
ACC CAC ACC GTC ACC TAT GGG AA ^t TC GAG GGC AAT GCC GCC AAG AGG Thr His Thr Val Thr Tyr Gly Asn Ile Glu Gly Asn Ala Ala Lys Arg 1065 1070 1075 1080	3449
CGT AAG CAG CAA TAT AAG GAC AGC CTG AAG AAG CGG CCT GCC TCG GCC Arg Lys Gln Gln Tyr Lys Asp Ser Leu Lys Lys Arg Pro Ala Ser Ala 1085 1090 1095	3497
AAG TCC CGC AGG GAG TTT GAC GAG ATC GAG CTG GCC TAC CGT CGC CGA Lys Ser Arg Arg Glu Phe Asp Glu Ile Glu Leu Ala Tyr Arg Arg Arg 1100 1105 1110	3545
CCG CCC CGC TCC CCT GAC CAC AAG CGC TAC TTC AGG GAC AAG GAA GGG Pro Pro Arg Ser Pro Asp His Lys Arg Tyr Phe Arg Asp Lys Glu Gly 1115 1120 1125	3593
CTA CGG GAC TTC TAC CTG GAC CAG TTC CGA ACA AAG GAG AAC TCA CCC Leu Arg Asp Phe Tyr Leu Asp Gln Phe Arg Thr Lys Glu Asn Ser Pro 1130 1135 1140	3641
CAC TGG GAG CAC GTA GAC CTG ACC GAC ATC TAC AAG GAG CGG AGT GAT His Trp Glu His Val Asp Leu Thr Asp Ile Tyr Lys Glu Arg Ser Asp 1145 1150 1155 1160	3689
GAC TTT AAG CGC GAC TCC ATC AGC GGA GGA GGG CCC TGT ACC AAC AGG Asp Phe Lys Arg Asp Ser Ile Ser Gly Gly Pro Cys Thr Asn Arg 1165 1170 1175	3737
TCT CAC ATC AAG CAC GGG ACG GGC GAC AAA CAC GGC GTG GTC AGC GGG Ser His Ile Lys His Gly Thr Gly Asp Lys His Gly Val Val Ser Gly 1180 1185 1190	3785
GTA CCT GCA CCT TGG GAG AAG AAC CTG ACC AAC GTG GAG TGG GAG GAC Val Pro Ala Pro Trp Glu Lys Asn Leu Thr Asn Val Glu Trp Glu Asp 1195 1200 1205	3833
CGG TCC GGG GGC AAC TTC TGC CGC AGC TGT CCC TCC AAG CTG CAC AAC Arg Ser Gly Gly Asn Phe Cys Arg Ser Cys Pro Ser Lys Leu His Asn 1210 1215 1220	3881

TAC TCC ACG ACG GTG ACG GGT CAG AAC TCG GGC AGG CAG GCG TGC ATC Tyr Ser Thr Thr Val Thr Gly Gln Asn Ser Gly Arg Gln Ala Cys Ile 1225 1230 1235 1240	3929
CGG TGT GAG GCT TGC AAG AAA GCA GGC AAC CTG TAT GAC ATC ACT GAG Arg Cys Glu Ala Cys Lys Ala Gly Asn Leu Tyr Asp Ile Ser Glu 1245 1250 1255	3977
GAC AAC TCC CTG CAG GAA CTG GAC CAG CCG GCT GCC CCA GTG GCG GTG Asp Asn Ser Leu Gln Glu Leu Asp Gln Pro Ala Ala Pro Val Ala Val 1260 1265 1270	4025
ACG TCA AAC GCC TCC ACC ACT AAG TAC CCT CAG AGC CCG ACT AAT TCC Thr Ser Asn Ala Ser Thr Thr Lys Tyr Pro Gln Ser Pro Thr Asn Ser 1275 1280 1285	4073
AAG GCC CAG AAG AAC CGG AAC AAA CTG CGC CGG CAG CAC TCC TAC Lys Ala Gln Lys Lys Asn Arg Asn Lys Leu Arg Arg Gln His Ser Tyr 1290 1295 1300	4121
GAC ACC TTC GTG GAC CTG CAG AAG GAA GAA GCC GCC CTG GCC CCG CGC Asp Thr Phe Val Asp Leu Gln Lys Glu Glu Ala Ala Leu Ala Pro Arg 1305 1310 1315 1320	4169
AGC GTA AGC CTG AAA GAC AAG GGC CGA TTC ATG GAT GGG AGC CCC TAC Ser Val Ser Leu Lys Asp Lys Gly Arg Phe Met Asp Gly Ser Pro Tyr 1325 1330 1335	4217
GCC CAC ATG TTT GAG ATG TCA GCT GGC GAG AGC ACC TTT GCC AAC AAC Ala His Met Phe Glu Met Ser Ala Gly Glu Ser Thr Phe Ala Asn Asn 1340 1345 1350	4265
AAG TCC TCA GTG CCC ACT GCC GGA CAT CAC CAC AAC AAC CCC GGC Lys Ser Ser Val Pro Thr Ala Gly His His His His Asn Asn Pro Gly 1355 1360 1365	4313
GGC GGG TAC ATG CTC AGC AAG TCG CTC TAC CCT GAC CGG GTC ACG CAA Gly Gly Tyr Met Leu Ser Lys Ser Leu Tyr Pro Asp Arg Val Thr Gln 1370 1375 1380	4361
AAC CCT TTC ATC CCC ACT TTT GGG GAC GAC CAG TGC TTG CTC CAT GGC Asn Pro Phe Ile Pro Thr Phe Gly Asp Asp Gln Cys Leu Leu His Gly 1385 1390 1395 1400	4409
AGC AAA TCC TAC TTC TTC AGG CAG CCC ACG GTG GCG GGG GCG TCG AAA Ser Lys Ser Tyr Phe Phe Arg Gln Pro Thr Val Ala Gly Ala Ser Lys 1405 1410 1415	4457
GCC AGG CCG GAC TTC CGG GCC CTT GTC ACC AAC AAG CCG GTG GTC TCG Ala Arg Pro Asp Phe Arg Ala Leu Val Thr Asn Lys Pro Val Val Ser 1420 1425 1430	4505
GCC CTT CAT GGG GCC GTG CCA GCC CGT TTC CAG AAG GAC ATC TGT ATA Ala Leu His Gly Ala Val Pro Ala Arg Phe Gln Lys Asp Ile Cys Ile 1435 1440 1445	4553
GGG AAC CAG TCC AAC CCC TGT GTG CCT AAC AAC ACA AAC CCC AGG GCT Gly Asn Gln Ser Asn Pro Cys Val Pro Asn Asn Thr Asn Pro Arg Ala 1450 1455 1460	4601
TTC AAT GGC TCC AGC AAT GGG CAT GTT TAT GAG AAA CTT TCT AGT ATT Phe Asn Gly Ser Ser Asn Gly His Val Tyr Glu Lys Leu Ser Ser Ile 1465 1470 1475 1480	4649
GAG TCT GAT GTC TGAGTGAGGG AACAGAGAGG TTAAGGTGGG TACGGGAGGG Glu Ser Asp Val	4701

TAAGGCTGTG GGT CGCGTGA TCGC CATGTC ACGGAGGGTG ACGGGGTGA ACTTGGTTCC	4761
CATTTGCTCC TTTCTTGT TTAA TTTATTT ATGGGATCCT GGAGTTCTGG TTCCTACTGG	4821
GGGCAACCT GGTGACCAGC ACCATCTCTC CTCCCTTCA CAGTTCTCTC CTTCTTCCCC	4881
CCGCTGTCAG CCATT CCTGT TCCC ATGAGA TGATGCCATG GGCCCTCTCA GCAGGGGAGG	4941
GTAGAGCGGA GAAAGGAAGG GCTGCATGCC GGCTTCCCTCC TGGTGTGGAA GAGCTCCTTG	5001
ATAT CCTCTT TGAGTGAAGC TGGGAGAACC AAAAAGAGGC TATGTGAGCA CAAAGGTAGC	5061
TTTTCCAAA CTGATCTTTT CATT TAGGTG AGGAAGCAA AGCATCTATG TGAGACCATT	5121
TAGCACACTG CTT GTGAAAG GAAAGAGGCT CTGGCTAAAT TCATGCTGCT TAGATGACAT	5181
CTGTCTAGGA ATCATGTGCC AAGCAGAGGT TGGGAGGCCA TTTGTGTTA TATATAAGCC	5241
AAAAATGCT TGCTTCAACC CCATGAGACT CGATAGTGGT GGTGAACAGA ACCCAAGGTC	5301
ATTGGTGGCA GAGTGGATTG TTGAACAAAC TGGAAAGTAC GTTATGATAG TGTCCCCCGG	5361
TGCCTTGGGG ACAAGAGCAG GTGGATTGTG CGTGCATGTG TGTTCATGCA CACTTGCACC	5421
CATGTGTAGT CAGGTGCCTC AAGAGAAGGC AACCTTGACT CTTTCGTTGA ATTTGCATCT	5481
CTTCAAGACA CAAGATTAAA ACAAAATTTA CGCTAAATTG GATTTAAAT TATCTTC	5538

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Pro Arg Ala Glu Cys Cys Ser Pro Lys Phe Trp Leu Val Leu	
1 5 10 15	
Ala Val Leu Ala Val Ser Gly Ser Arg Ala Arg Ser Gln Lys Ser Pro	
20 25 30	
Pro Ser Ile Gly Ile Ala Val Ile Leu Val Gly Thr Ser Asp Glu Val	
35 40 45	
Ala Ile Lys Asp Ala His Glu Lys Asp Asp Phe His His Leu Ser Val	
50 55 60	
Val Pro Arg Val Glu Leu Val Ala Met Asn Glu Thr Asp Pro Lys Ser	
65 70 75 80	
Ile Ile Thr Arg Ile Cys Asp Leu Met Ser Asp Arg Lys Ile Gln Gly	
85 90 95	
Val Val Phe Ala Asp Asp Thr Asp Gln Glu Ala Ile Ala Gln Ile Leu	
100 105 110	
Asp Phe Ile Ser Ala Gln Thr Leu Thr Pro Ile Leu Gly Ile His Gly	
115 120 125	
Gly Ser Ser Met Ile Met Ala Asp Lys Asp Glu Ser Ser Met Phe Phe	
130 135 140	

Gln Phe Gly Pro Ser Ile Glu Gln Gln Ala Ser Val Met Leu Asn Ile
 145 150 155 160
 Met Glu Glu Tyr Asp Trp Tyr Ile Phe Ser Ile Val Thr Thr Tyr Phe
 165 170 175
 Pro Gly Tyr Gln Asp Phe Val Asn Lys Ile Arg Ser Thr Ile Glu Asn
 180 185 190
 Ser Phe Val Gly Trp Glu Leu Glu Val Leu Leu Leu Asp Met Ser
 195 200 205
 Leu Asp Asp Gly Asp Ser Lys Ile Gln Asn Gln Leu Lys Lys Leu Gln
 210 215 220
 Ser Pro Ile Ile Leu Leu Tyr Cys Thr Lys Glu Glu Ala Thr Tyr Ile
 225 230 235 240
 Phe Glu Val Ala Asn Ser Val Gly Leu Thr Gly Tyr Gly Tyr Thr Trp
 245 250 255
 Ile Val Pro Ser Leu Val Ala Gly Asp Thr Asp Thr Val Pro Ala Glu
 260 265 270
 Phe Pro Thr Gly Leu Ile Ser Val Ser Tyr Asp Glu Trp Asp Tyr Gly
 275 280 285
 Leu Pro Pro Arg Val Arg Asp Gly Ile Ala Ile Ile Thr Thr Ala Ala
 290 295 300
 Ser Asp Met Leu Ser Glu His Ser Phe Ile Pro Glu Pro Lys Ser Ser
 305 310 315 320
 Cys Tyr Asn Thr His Glu Lys Arg Ile Tyr Gln Ser Asn Met Leu Asn
 325 330 335
 Arg Tyr Leu Ile Asn Val Thr Phe Glu Gly Arg Asn Leu Ser Phe Ser
 340 345 350
 Glu Asp Gly Tyr Gln Met His Pro Lys Leu Val Ile Ile Leu Leu Asn
 355 360 365
 Lys Glu Arg Lys Trp Glu Arg Val Gly Lys Trp Lys Asp Lys Ser Leu
 370 375 380
 Gln Met Lys Tyr Tyr Val Trp Pro Arg Met Cys Pro Glu Thr Glu Glu
 385 390 395 400
 Gln Glu Asp Asp His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe
 405 410 415
 Val Ile Val Glu Ser Val Asp Pro Leu Ser Gly Thr Cys Met Arg Asn
 420 425 430
 Thr Val Pro Cys Gln Lys Arg Ile Val Thr Glu Asn Lys Thr Asp Glu
 435 440 445
 Glu Pro Gly Tyr Ile Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile
 450 455 460
 Leu Lys Lys Ile Ser Lys Ser Val Lys Phe Thr Tyr Asp Leu Tyr Leu
 465 470 475 480
 Val Thr Asn Gly Lys His Gly Lys Lys Ile Asn Gly Thr Trp Asn Gly
 485 490 495

Met Ile Gly Glu Val Val Met Lys Arg Ala Tyr Met Ala Val Gly Ser
 500 505 510
 Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro
 515 520 525
 Phe Ile Glu Thr Gly Ile Ser Val Me Val Ser Arg Ser Asn Gly Thr
 530 535 540
 Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Asp Val Trp Val
 545 550 555 560
 Met Met Phe Val Met Leu Leu Ile Val Ser Ala Val Ala Val Phe Val
 565 570 575
 Phe Glu Tyr Phe Ser Pro Val Gly Tyr Asn Arg Cys Leu Ala Asp Gly
 580 585 590
 Arg Glu Pro Gly Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu
 595 600 605
 Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys
 610 615 620
 Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val
 625 630 635 640
 Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln
 645 650 655
 Glu Glu Tyr Val Asp Gln Val Ser Gly Leu Ser Asp Lys Lys Phe Gln
 660 665 670
 Arg Pro Asn Asp Phe Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn
 675 680 685
 Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Ala Glu Met His Ala
 690 695 700
 Tyr Met Gly Lys Phe Asn Gln Arg Gly Val Asp Asp Ala Leu Leu Ser
 705 710 715 720
 Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu
 725 730 735
 Asn Tyr Met Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly
 740 745 750
 Ser Gly Lys Val Phe Ala Ser Thr Gly Tyr Gly Ile Ala Ile Gln Lys
 755 760 765
 Asp Ser Gly Trp Lys Arg Gln Val Asp Leu Ala Ile Leu Gln Leu Phe
 770 775 780
 Gly Asp Gly Glu Met Glu Glu Leu Glu Ala Leu Trp Leu Thr Gly Ile
 785 790 795 800
 Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp
 805 810 815
 Asn Met Ala Gly Val Phe Tyr Met Leu Gly Ala Ala Met Ala Leu Ser
 820 825 830
 Leu Ile Thr Phe Ile Cys Glu His Leu Phe Tyr Trp Gln Phe Arg His
 835 840 845

Cys Phe Met Gly Val Cys Ser Gly Lys Pro Gly Met Val Phe Ser Ile
 850 855 860
 Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val Ala Ile Glu Glu Arg
 865 870 875 880
 Gln Ser Val Met Asn Ser Pro Thr Ala Thr Met Asn Asn Thr His Ser
 885 890 895
 Asn Ile Leu Arg Leu Leu Arg Thr Ala Lys Asn Met Ala Asn Leu Ser
 900 905 910
 Gly Val Asn Gly Ser Pro Gln Ser Ala Leu Asp Phe Ile Arg Arg Glu
 915 920 925
 Ser Ser Val Tyr Asp Ile Ser Glu His Arg Arg Ser Phe Thr His Ser
 930 935 940
 Asp Cys Lys Ser Tyr Asn Asn Pro Pro Cys Glu Glu Asn Leu Phe Ser
 945 950 955 960
 Asp Tyr Ile Ser Glu Val Glu Arg Thr Phe Gly Asn Leu Gln Leu Lys
 965 970 975
 Asp Ser Asn Val Tyr Gln Asp His Tyr His His His His Arg Pro His
 980 985 990
 Ser Ile Gly Ser Ala Ser Ser Ile Asp Gly Leu Tyr Asp Cys Asp Asn
 995 1000 1005
 Pro Pro Phe Thr Thr Gln Ser Arg Ser Ile Ser Lys Lys Pro Leu Asp
 1010 1015 1020
 Ile Gly Leu Pro Ser Ser Lys His Ser Gln Leu Ser Asp Leu Tyr Gly
 1025 1030 1035 1040
 Lys Phe Ser Phe Lys Ser Asp Arg Tyr Ser Gly His Asp Asp Leu Ile
 1045 1050 1055
 Arg Ser Asp Val Ser Asp Ile Ser Thr His Thr Val Thr Tyr Gly Asn
 1060 1065 1070
 Ile Glu Gly Asn Ala Ala Lys Arg Arg Lys Gln Gln Tyr Lys Asp Ser
 1075 1080 1085
 Leu Lys Lys Arg Pro Ala Ser Ala Lys Ser Arg Arg Glu Phe Asp Glu
 1090 1095 1100
 Ile Glu Leu Ala Tyr Arg Arg Arg Pro Pro Arg Ser Pro Asp His Lys
 1105 1110 1115 1120
 Arg Tyr Phe Arg Asp Lys Glu Gly Leu Arg Asp Phe Tyr Leu Asp Gln
 1125 1130 1135
 Phe Arg Thr Lys Glu Asn Ser Pro His Trp Glu His Val Asp Leu Thr
 1140 1145 1150
 Asp Ile Tyr Lys Glu Arg Ser Asp Asp Phe Lys Arg Asp Ser Ile Ser
 1155 1160 1165
 Gly Gly Gly Pro Cys Thr Asn Arg Ser His Ile Lys His Gly Thr Gly
 1170 1175 1180
 Asp Lys His Gly Val Val Ser Gly Val Pro Ala Pro Trp Glu Lys Asn
 1185 1190 1195 1200

Leu Thr Asn Val Glu Trp Glu Asp Arg Ser Gly Gly Asn Phe Cys Arg
 1205 1210 1215
 Ser Cys Pro Ser Lys Leu His Asn Tyr Ser Thr Thr Val Thr Gly Gln
 1220 1225 1230
 Asn Ser Gly Arg Gln Ala Cys Ile Arg Cys Glu Ala Cys Lys Ala
 1235 1240 1245
 Gly Asn Leu Tyr Asp Ile Ser Glu Asp Asn Ser Leu Gln Glu Leu Asp
 1250 1255 1260
 Gln Pro Ala Ala Pro Val Ala Val Thr Ser Asn Ala Ser Thr Thr Lys
 1265 1270 1275 1280
 Tyr Pro Gln Ser Pro Thr Asn Ser Lys Ala Gln Lys Lys Asn Arg Asn
 1285 1290 1295
 Lys Leu Arg Arg Gln His Ser Tyr Asp Thr Phe Val Asp Leu Gln Lys
 1300 1305 1310
 Glu Glu Ala Ala Leu Ala Pro Arg Ser Val Ser Leu Lys Asp Lys Gly
 1315 1320 1325
 Arg Phe Met Asp Gly Ser Pro Tyr Ala His Met Phe Glu Met Ser Ala
 1330 1335 1340
 Gly Glu Ser Thr Phe Ala Asn Asn Lys Ser Ser Val Pro Thr Ala Gly
 1345 1350 1355 1360
 His His His Asn Asn Pro Gly Gly Tyr Met Leu Ser Lys Ser
 1365 1370 1375
 Leu Tyr Pro Asp Arg Val Thr Gln Asn Pro Phe Ile Pro Thr Phe Gly
 1380 1385 1390
 Asp Asp Gln Cys Leu Leu His Gly Ser Lys Ser Tyr Phe Phe Arg Gln
 1395 1400 1405
 Pro Thr Val Ala Gly Ala Ser Lys Ala Arg Pro Asp Phe Arg Ala Leu
 1410 1415 1420
 Val Thr Asn Lys Pro Val Val Ser Ala Leu His Gly Ala Val Pro Ala
 1425 1430 1435 1440
 Arg Phe Gln Lys Asp Ile Cys Ile Gly Asn Gln Ser Asn Pro Cys Val
 1445 1450 1455
 Pro Asn Asn Thr Asn Pro Arg Ala Phe Asn Gly Ser Ser Asn Gly His
 1460 1465 1470
 Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val
 1475 1480

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4695 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 485..4495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGAGAACACA GCGAGTGTGT GAGTCCCTCC CGCTCCAGCT CCTCCAAGCC CGGGCCGCCG	60
CCGCCACCCCT CGCCCGCAGC CTCCCGCAGC CTCCCTCGGC CACCGGTGTC TGGTGGGGGT	120
GTTGCCTGGG TAGGTCGGCC CGGCCCCCAG GGGTCTCTCG AGCGTCTGCC ATCTGCCCGA	180
GAAACATGTG TGGCCACGTC CTCGCCTAGT CCAGGTGGCC GCAACCTTGG GGGAGAGACA	240
GGGCAGGACA GGACCAAGGT AAGAGGTAAG GAGGAGACGG CGCCAGGGAC AGACAGGAGG	300
TCCCAGGCTTG CCGTTGTGCG CACCACCACT GCCGCCGCC CGGGGCCTGC CCCCGACATC	360
GGCTCTCTGA GCCCTCCTCG GAATCTTGGG GTCGCTGGAC GCCGGGTTCC GGTCTGGCC	420
CCCCCGCCAT CCCCCCAACA GAACAGGGTC ATGAAAAGAG GCGGCCCGGC GGGGCCCGCA	480
GGCG ATG CGC GGC GCC GGT GGC CCC CGC GGC CCT CGG GGC CCC GCT AAG Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys	529
1 5 10 15	
ATG CTG CTG CTG CTG GCG CTG GCC TGC GCC AGC CCG TTC CCG GAG GAG Met Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu	577
20 25 30	
GCG CCG GGG CCG GGC GGG GGT GGG CCC GGC GGC GGC CTC GGC GGG Ala Pro Gly Pro Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly	625
35 40 45	
GCG CGG CCG CTC AAC GTG GCG CTC GTG TTC TCG GGG CCC GCG TAC GCG Ala Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala	673
50 55 60	
GCC GAG GCG GCA CGC CTG GGC CCG GCC GTG GCG GCG GCG GTG CGC AGC Ala Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser	721
65 70 75	
CCG GGC CTA GAC GTG CGG CCC GTG GCG CTG GTG CTC AAC GGC TCG GAC Pro Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp	769
80 85 90 95	
CCG CGC AGC CTC GTG CTG CAG CTC TGC GAC CTG CTG TCG GGG TTG CGC Pro Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg	817
100 105 110	
GTG CAC GGC GTG GTC TTC GAA GAC GAC TCG CGC GCG CCC GCC GTC GCG Val His Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala	865
115 120 125	
CCC ATC CTC GAC TTC CTG TCG GCG CAG ACC TCG CTC CCC ATC GTG TCC Pro Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser	913
130 135 140	
GAG CAC GGC GGC GCC GCG CTC GTG CTC ACG CCC AAG GAG AAG GGC TCC Glu His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser	961
145 150 155	
ACC TTC CTC CAC CTG GGC TCT TCC CCC GAG CAA CAG CTT CAG GTC ATC Thr Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile	1009
160 165 170 175	

TTT GAG GTG CTG GAG GAG TAT GAC TGG ACG TCC TTT GTA GCC GTG ACC Phe Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr 180 185 190	1057
ACT CGT GCC CCT GGC CAC CGG GCC TTC CTG TCC TAC ATT GAG GTG CTG Thr Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu 195 200 205	1105
ACT GAC GGC AGT CTG GTG GGC TGG GAG CAC CGC GGA GCG CTG ACG CTG Thr Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu 210 215 220	1153
GAC CCT GGG GCG GGC GAG GCC GTG CTC AGT GCC CAG CTC CGC AGT GTC Asp Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val 225 230 235	1201
AGC GCG CAG ATC CGC CTG CTC TTC TGC GCC CGA GAG GAG GCC GAG CCC Ser Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro 240 245 250 255	1249
GTG TTC CGC GCA GCT GAG GAG GCT GGC CTC ACT GGA TCT GGC TAC GTC Val Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val 260 265 270	1297
TGG TTC ATG GTG GGG CCC CAG CTG GCT GGA GGC GGG GGC TCT GGG GCC Trp Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Ser Gly Ala 275 280 285	1345
CCT GGT GAG CCC CCT CTT CTG CCA GGA GGC GCC CCC CTG CCT GCC GGG Pro Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly 290 295 300	1393
CTG TTT GCA GTG CGC TCG GCT GGG CGG GAT GAC CTG GCT CGG CGA Leu Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg 305 310 315	1441
GTG GCA GCT GGC GTG GCC GTA GTG GCC AGA GGT GCC CAG GCC CTG CTG Val Ala Ala Gly Val Ala Val Ala Arg Gly Ala Gln Ala Leu Leu 320 325 330 335	1489
CGT GAT TAT GGT TTC CTT CCT GAG CTC GGC CAC GAC TGT CGC GCC CAG Arg Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln 340 345 350	1537
AAC CGC ACC CAC CGC GGG GAG AGT CTG CAT AGG TAC TTC ATG AAC ATC Asn Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile 355 360 365	1585
ACG TGG GAT AAC CGG GAT TAC TCC TTC AAT GAG GAC GGC TTC CTA GTG Thr Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val 370 375 380	1633
AAC CCC TCC CTG GTG GTC ATC TCC CTC ACC AGA GAC AGG ACG TGG GAG Asn Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu 385 390 395	1681
GTG GTG GGC AGC TGG GAG CAG CAG ACG CTC CGC CTC AAG TAC CCG CTG Val Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu 400 405 410 415	1729
TGG TCC CGC TAT GGT CGC TTC CTG CAG CCA GTG GAC GAC ACG CAG CAC Trp Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His 420 425 430	1777
CTC GCG GTG GCC ACG CTG GAG GAA AGG CCG TTT GTC ATC GTG GAG CCT Leu Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro 435 440 445	1825

GCA GAC CCT ATC AGC GCC ACC TGC ATC CGA GAC TCC GTC CCC TGC CGG Ala Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg 450 455 460	1873
AGC CAG CTC AAC CGA ACC CAC AGC CCT CCA CCG GAT GCC CCC CGC CCG Ser Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro 465 470 475	1921
GAA AAG CGC TGC TGC AAG GGT TTC TGC ATC GAC ATT CTG AAG CGG CTG Glu Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu 480 485 490 495	1969
GCG CAT ACC ATC GGC TTC AGC TAC GAC CTC TAC CTG GTC ACC AAT GGC Ala His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly 500 505 510	2017
AAG CAC GGA AAG AAG ATC GAT GGC GTC TGG AAC GGC ATG ATC GGG GAG Lys His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu 515 520 525	2065
GTG TTC TAC CAG CGC GCA GAC ATG GCC ATC GGC TCC CTC ACC ATC AAC Val Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn 530 535 540	2113
GAG GAG CGC TCC GAG ATC GTG GAC TTC TCC GTC CCC TTC GTG GAG ACC Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr 545 550 555	2161
GGC ATC AGC GTC ATG GTG GCG CGC AGC AAT GGC ACG GTG TCC CCC TCG Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser 560 565 570 575	2209
GCC TTC CTC GAG CCC TAC AGC CCC GCC GTG TGG GTG ATG ATG TTC GTC Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val 580 585 590	2257
ATG TGC CTC ACT GTG GTC GCC GTC ACT GTT TTC ATC TTC GAG TAC CTC Met Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu 595 600 605	2305
AGT CCT GTT GGT TAC AAC CGC AGC CTG GCC ACG GGC AAG CGC CCT GGC Ser Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly 610 615 620	2353
GGT TCA ACC TTC ACC ATT GGG AAA TCC ATC TGG CTG CTC TGG GCC CTG Gly Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu 625 630 635	2401
GTG TTC AAT AAT TCG GTG CCC GTG GAG AAC CCC CGG GGA ACC ACC AGC Val Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser 640 645 650 655	2449
AAA ATC ATG GTG CTG GTG TGG GCC TTC TCC GCC GTC ATC TTC CTC GCC Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala 660 665 670	2497
AGC TAC ACA GCC AAC CTG GCC GCC TTC ATG ATC CAG GAG GAG TAC GTG Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val 675 680 685	2545
GAT ACT GTG TCT GGG CTC AGT GAC CGC AAG TTC CAG AGG CCC CAG GAG Asp Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu 690 695 700	2593
CAG TAC CCG CCC CTG AAG TTT GGG ACC GTG CCC AAC GGC TCC ACG GAG Gln Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu 705 710 715	2641

AAG AAC ATC CGC AGC AAC TAT CCC GAC ATG CAC AGC TAC ATG GTG CGC Lys Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg 720 725 730 735	2689
TAC AAC CAG CCC CGC GTA GAG GAA GCG CTC ACT CAG CTC AAG GCA GGG Tyr Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly 740 745 750	2737
AAG CTG GAC GCC TTC ATC TAC GAT GCT GCA GTG CTC AAT TAC ATG GCC Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala 755 760 765	2785
CGC AAG GAC GAG GGC TGC AAG CTT GTC ACC ATC GGC TCC GGC AAG GTC Arg Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val 770 775 780	2833
TTC GCC ACG ACA GGC TAT GGC ATC GCC CTG CAC AAG GGC TCC CGC TGG Phe Ala Thr Thr Gly Tyr Ile Ala Leu His Lys Gly Ser Arg Trp 785 790 795	2881
AAG CGG CCC ATC GAC CTG GCG TTG CTG CAG TTC CTG GGG GAT GAT GAG Lys Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu 800 805 810 815	2929
ATC GAG ATG CTG GAG CGG CTG TGG CTC TCT GGG ATC TGC CAC AAT GAC Ile Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp 820 825 830	2977
AAA ATC GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC ATG GCG GGC Lys Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly 835 840 845	3025
GTC TTC TAC ATG CTC CTG GTG GCC ATG GGC CTG TCC CTG CTG GTC TTC Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe 850 855 860	3073
GCC TGG GAG CAC CTG GTG TAC TGG CGC CTG CGG CAC TGC CTG GGG CCC Ala Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro 865 870 875	3121
ACC CAC CGC ATG GAC TTC CTG CTG GCC TTC TCC AGG GGC ATG TAC AGC Thr His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser 880 885 890 895	3169
TGC TGC AGC GCT GAG GCC GCC CCA CCG CCC GCC AAG CCC CCG CCG CCG Cys Cys Ser Ala Glu Ala Ala Pro Pro Ala Lys Pro Pro Pro Pro 900 905 910	3217
CCA CAG CCC CTG CCC AGC CCC GCG TAC CCC GCG CCG GGG CCG GCT CCC Pro Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro 915 920 925	3265
GGG CCC GCA CCT TTC GTC CCC CGC GAG CGC GCC TCA GTG GCC CGC TGG Gly Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp 930 935 940	3313
CGC CGG CCC AAG GGC GCG GGG CCG CCG GGG GGC GCG GGC CTG GCC GAC Arg Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp 945 950 955	3361
GGC TTC CAC CGC TAC TAC GGC CCC ATC GAG CCG CAG GGC CTA GGC CTC Gly Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu 960 965 970 975	3409
GGC CTG GGC GAA GCG CGC GCG GCA CCG CGG GGC GCA GGC GGG CGC CCG Gly Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro 980 985 990	3457

CTG TCC CCG CCG GCC GCT CAG CCC CCG CAG AAG CCG CCG GCC TCC TAT Leu Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr 995 1000 1005	3505
TTC GCC ATC GTA CGC GAC AAG GAG CCA GCC GAG CCC CCC GCC GCC GCC Phe Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala 1010 1015 1020	3553
TTC CCC GGC TTC CCG TCC CCG CCC GCG CCC CCC GCC GCC GCG GCC ACC Phe Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Thr 1025 1030 1035	3601
GCC GTC GGG CCG CCA CTC TGC CGC TTG GCC TTC GAG GAC GAG AGC CCG Ala Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro 1040 1045 1050 1055	3649
CCG GCG CCC GCG CGG TGG CCG CGC TCG GAC CCC GAG AGC CAA CCC CTG Pro Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu 1060 1065 1070	3697
CTG GGG CCA GGC GCG GGC GCG GGG GGC ACG GGG GGC GCA GGC GGA Leu Gly Pro Gly Ala Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly 1075 1080 1085	3745
GGA GCC CCG GCC GCT CCG CCC CCG TGC TTC GCC GCG CCG CCC CCG TGC Gly Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys 1090 1095 1100	3793
TTT TAC CTC GAT GTC GAC CAG TCG CCG TCG GAC TCG GAG GAC TCG GAG Phe Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu 1105 1110 1115	3841
AGC CTG GCC GGC GCG TCC CTG GCC GGC CTG GAT CCC TGG TGG TTC GCC Ser Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala 1120 1125 1130 1135	3889
GAC TTC CCT TAC CCG TAT GCC GAT CGC CTC GGG CSG CCC GCG GCA CGC Asp Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg 1140 1145 1150	3937
TAC GGA TTG GTC GAC AAA CTA GGG GGC TGG CTC GCC GGG AGC TGG GAC Tyr Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp 1155 1160 1165	3985
TAC CTG CCT CCS CGC AGC GGT CGG GCC TGG CAC TGT CGG CAC TGC Tyr Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys 1170 1175 1180	4033
GCC AGC CTG GAG CTG CTT CCG CCG CCG CGC CAT CTC AGC TGC TCG CAC Ala Ser Leu Glu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His 1185 1190 1195	4081
GAT GGC CTG GAC GGC GGC TGG TGG GCG CCA CCG CCT CCA CCC TGG GCC Asp Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Trp Ala 1200 1205 1210 1215	4129
GCC GGG CCC CTG CCC CGA CGC CGG GCC CGC TGC GGG TGC CCG CGG TCG Ala Gly Pro Leu Pro Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser 1220 1225 1230	4177
CAC CCG CAC CGC CCG CGG GCC TCG CAC CGC ACG CCC GCC GCT GCC CGG His Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala 1235 1240 1245	4225
CCC CAC CAC CAC AGG CAC CGG CGC GCC GCT GGG GGC TGG GAC CTC CCG Pro His His His Arg His Arg Ala Ala Gly Gly Trp Asp Leu Pro 1250 1255 1260	4273

135

CCG CCC GCG CCC ACC TCG CGC TCG CTC GAG GAC CTC AGC TCG TGC CCT Pro Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro	4321
1265 1270 1275	
CGC GCC CCT GCG CGC AGG CTT ACC GGG CCC TCC CGC CAC GCT CGC Arg Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg	4369
1280 1285 1290 1295	
AGG TGT CCG CAC GCC GCG CAC TGG GGG CCG CCG CTG CCT ACA GCT TCC Arg Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser	4417
1300 1305 1310	
CAC CGG AGA CAC CGG GGC GGG GAC CTG GGC ACC CGC AGG GGC TCG GCG His Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala	4465
1315 1320 1325	
CAC TTC TCT AGC CTC GAG TCC GAG GTA TGACGGGCC CCGGGGGCCC His Phe Ser Ser Leu Glu Ser Glu Val	4512
1330 1335	
CACCGCCCCC TTGGTCAGCG CAGGCCACGG CCCGAGGGGG CGCCCGCAGT GGACAGGACC	4572
CGCGTGGGTT GGGAAAGGAAA GCAGTGGAAC TGGCCGGACC CCGCCTGGAG CAGCGTCCTG	4632
CGCCCCCTGG TTCTGGAGGA ACCGCAAGCC GGAGAGGATT TGGTCCCTCA ACTATCACCC	4692
AGG	4695

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1336 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys Met	
1 5 10 15	
Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu Ala	
20 25 30	
Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly Ala	
35 40 45	
Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala Ala	
50 55 60	
Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser Pro	
65 70 75 80	
Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp Pro	
85 90 95	
Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg Val	
100 105 110	
His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala Pro	
115 120 125	
Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser Glu	
130 135 140	

His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser Thr
 145 150 155 160
 Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile Phe
 165 170 175
 Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr Thr
 180 185 190
 Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu Thr
 195 200 205
 Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu Asp
 210 215 220
 Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val Ser
 225 230 235 240
 Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro Val
 245 250 255
 Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val Trp
 260 265 270
 Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Ser Gly Ala Pro
 275 280 285
 Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly Leu
 290 295 300
 Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg Val
 305 310 315 320
 Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu Arg
 325 330 335
 Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln Asn
 340 345 350
 Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile Thr
 355 360 365
 Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val Asn
 370 375 380
 Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu Val
 385 390 395 400
 Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu Trp
 405 410 415
 Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His Leu
 420 425 430
 Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro Ala
 435 440 445
 Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg Ser
 450 455 460
 Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro Glu
 465 470 475 480
 Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu Ala
 485 490 495

His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys
 500 505 510
 His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu Val
 515 520 525
 Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu
 530 535 540
 Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly
 545 550 555 560
 Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala
 565 570 575
 Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val Met
 580 585 590
 Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu Ser
 595 600 605
 Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly Gly
 610 615 620
 Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu Val
 625 630 635 640
 Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser Lys
 645 650 655
 Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser
 660 665 670
 Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp
 675 680 685
 Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu Gln
 690 695 700
 Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Lys
 705 710 715 720
 Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg Tyr
 725 730 735
 Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly Lys
 740 745 750
 Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Arg
 755 760 765
 Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe
 770 775 780
 Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp Lys
 785 790 795 800
 Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu Ile
 805 810 815
 Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp Lys
 820 825 830
 Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly Val
 835 840 845

Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe Ala
 850 855 860
 Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro Thr
 865 870 875 880
 His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser Cys
 885 890 895
 Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro Pro
 900 905 910
 Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro Gly
 915 920 925
 Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp Arg
 930 935 940
 Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp Gly
 945 950 955 960
 Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu Gly
 965 970 975
 Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro Leu
 980 985 990
 Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr Phe
 995 1000 1005
 Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala Phe
 1010 1015 1020
 Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Ala Thr Ala
 1025 1030 1035 1040
 Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro Pro
 1045 1050 1055
 Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu Leu
 1060 1065 1070
 Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly Gly
 1075 1080 1085
 Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys Phe
 1090 1095 1100
 Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu Ser
 1105 1110 1115 1120
 Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala Asp
 1125 1130 1135
 Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg Tyr
 1140 1145 1150
 Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp Tyr
 1155 1160 1165
 Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys Ala
 1170 1175 1180
 Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His Asp
 1185 1190 1195 1200

Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Pro Trp Ala Ala
 1205 1210 1215
 Gly Pro Leu Pro Arg Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser His
 1220 1225 1230
 Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Ala Pro
 1235 1240 1245
 His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro Pro
 1250 1255 1260
 Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro Arg
 1265 1270 1275 1280
 Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg Arg
 1285 1290 1295
 Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser His
 1300 1305 1310
 Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala His
 1315 1320 1325
 Phe Ser Ser Leu Glu Ser Glu Val
 1330 1335

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGTGGCGGC CGCAGAGCAC CTCCACCATC TCCTTGTCT ACTCCAAGAT CTGGCCCTAG	60
TCCATGTTG C	71

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGGTGGTCCC CAACCTGTAG GACTTGGTTC TGGAGGAGGA TCTGGTGTAG GCAAACATGG	60
ACTAGGGCCA G	71

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGGGGACCA	CCAGATGGA	GGTAGAGCTG	CACTTGTACG	AAGAGCTCCA	CAACCACCTG	60
G						61

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGTGAGACGT	CAGACAAAGG	AGGCCAGGT	GTAGGTGGTC	TACCAGGTGG	TTGTGGAGCT	60
CT						62

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGCAGAGCA	CCTCCACCAT	CTCCTTGTCC	TACTCCAAGA	TCTGCCCTA	GTCCATGTTT	60
GCCTACACCA	GATCCTCCTC	CAGAACCAAG	TCCTACAGGT	TGGGGACCAC	CAGATGGAGG	120
TAGAGCTGCA	CTTGTACGAA	GAGCTCCACA	ACCACCTGGT	AGACCACCTA	CACCTGGGCC	180
TCCTTTGTCT	GACGT					195